

Amendments to the Specification:

A. Please replace the fifth full paragraph on page 5, with the following amended paragraph:
FIGS. 5.1 to 5.46 present the coordinates for the crystal structure of Aequorea-related green fluorescent protein S65T-(~~SEQ ID NOS:5,6~~) (SEQ ID NO:5).

B. Please replace Table B which starts at line 24 on page 30, with the following amended table:

TABLE B

	Original position and presumed role	Change to	Codon
L42	Aliphatic residue near C=N of chromophore	C, F, H, L, Q, R, W, Y, Z (SEQ ID NO:7)	5'YDS 3' 3'RHS 5'
V61	Aliphatic residue near central —CH= of chromophore	F, Y, H, C, L, R (SEQ ID NO:8)	YDC RHg
T62	Almost directly above center of chromophore bridge	A, V, F, S, (SEQ ID NO:9) D, E, H, K, N, Q (SEQ ID NO:10) F, Y, H, C, L, R (SEQ ID NO:8)	KYC MRg VAS BTS YDC RHg
V68	Aliphatic residue near carbonyl and G67	F, Y, H, L (SEQ ID NO:11)	YWC RWg
N121	Near C—N site of ring closure between T65 and G67	C, F, H, L, Q, R, W, Y, Z (SEQ ID NO:7)	YDS RHS
Y145	Packs near tyrosine ring of chromophore	W, C, F, L (SEQ ID NO:12) D, E, H, N, K, Q (SEQ ID NO:13)	TKS AMS VAS BTS
H148	H-bonds to phenolate oxygen	F, Y, N, I (SEQ ID NO:14) K, Q, R	WWC WWg MRg KYC
V150	Aliphatic residue near tyrosine ring of chromophore	F, Y, H, L (SEQ ID NO:11)	YWC RWg
F165	Packs near tyrosine ring	C, H, Q, R, W, Y, Z (SEQ ID NO:15)	YRS RYS
I167	Aliphatic residue near phenolate; I167T has effects	F, Y, H, L (SEQ ID NO:11)	YWC RWg
T203	H-bonds to phenolic oxygen of chromophore	F, H, L, Q, R, W, Y, Z (SEQ ID NO:16)	YDS RHS
E222	Protonation regulates ionization of	H, K, N, Q (SEQ ID)	MAS

	chromophore	NO:17)	KTS
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C. Please replace Table C which starts at line 1 page 32 with the following amended table:

TABLE C

	Original position and presumed role	Change to	Codon
Q69	Terminates chain of H-bonding waters	<u>K, R, E, G</u> (SEQ ID NO:18)	RRg YYC
Q94	H-bonds to carbonyl terminus of chromophore	<u>D, E, H, K, N, Q</u> (SEQ ID NO:10)	VAS BTS
Q183	Bridges Arg96 and center of chromophore bridge	<u>H, Y</u> <u>E, K</u>	YAC RTG RAg YTC
N185	Part of H-bond network near carbonyl of chromophore	<u>D, E, H, N, K, Q</u> (SEQ ID NO:13)	VAS BTS

D. Please replace Table D, which starts at line26, page 32, with the following amended table:

TABLE D

	Original position and presumed role	Change to	Codon
L220	Packs next to Glu222; to make GFP pH sensitive	<u>H, K, N, P, Q, T</u> (SEQ ID NO:19)	MMS KKS
V224	Packs next to Glu222; to make GFP pH sensitive	<u>H, K, N, P, Q, T</u> (SEQ ID NO:19) <u>C, F, H, L, Q, R, W, Y, Z</u> (SEQ ID NO:7)	MMS KKS YDS RHS